AMENDMENTS TO THE SPECIFICATION:

Please add the following new paragraph after the paragraph ending on line 1 of page 1:

--CROSS REFERENCE TO RELATED APPLICATIONS

This application is a division of co-pending Application No. 09/673,032, filed on December 6, 2000, Application No. 09/673,032 is the national phase of PCT International Application No. PCT/GB99/01085 filed on April 8, 1999 under 35 U.S.C. § 371. The entire contents of each of the above-identified applications are hereby incorporated by reference--

Replace the paragraph beginning at page 13, line 15, with the following rewritten paragraph:

--Figure 4 is a comparison of pig CD59 protein sequence (SEQ ID NO: 1) with that of human (SEQ ID NO: 20), rat (SEQ ID NO: 21) and mouse (SEQ ID NO: 22) CD59. Numbering refers to the predicted pig CD59 sequence, with the first residue of the mature protein known from protein sequencing to be L. Vertical lines (|) show identity of conserved residues between pig CD59 and other species.—-

Replace the paragraph beginning at page 12, line 22, with the following rewritten paragraph:

--Figure 2 is the nucleotide (SEQ ID NO: 2) and deduced amino acid (SEQ ID NO: 1) sequence of pig CD59. The numbers

below refer to the nucleotide sequence, the numbers on the right refer to the amino acid sequence. The first residue of the mature protein (L-1) is boxed. Potential N-glycosylation sites (N-X-S/T) are denoted by psi (Ψ). The arrow (↓) indicates the putative GPI-anchor addition site (S-73). The pig CD59 GenBank accession number is AF020302.--

Replace the paragraph beginning at page 16, line 1 with the following rewritten paragraph:

--Figure 14 shows the nucleotide sequence of two different clones of pig DAF, i.e. pDAF-7 and pDAF-14 (SEQ ID Nos. 15 and 16). The pDAF-7 cDNA sequence corresponds to SEQ ID No. 15. The pDAF-14 cDNA sequence corresponds to SEQ ID No. 16.--

Replace the paragraph beginning at Page 16, line 4 with the following rewritten paragraph:

--Figure 15 shows the predicted protein sequence of pig DAF from the nucleotide sequences of clones pDAF-7 and pDAF-14 in Figure 14. It also shows the alignment of the predicted protein sequence of clone pDAF-7 in alignment with the protein sequence of human DAF (SEQ ID Nos. 17, 18 and 19). The pDAF-7, predicted protein sequence corresponds to SEQ ID No. 17. The pDAF 14 predicted protein sequence corresponds to SEQ ID No.

18. The sequence shown in alignment with human DAF corresponds to SEQ ID No. 19.--

Replace the paragraph beginning at page 26, line 16, with the following rewritten paragraph:

--Degenerate primers A-PIG ($TG^{C}/_{T}TA^{C}/_{T}AA^{C}/_{T}TG^{C}/_{T}AT^{A}/C/_{T}AA$) (SEQ ID No. 3) and C-PIG ($AG^{G}/_{A}TC^{C}/_{T}T^{C}/_{T}^{C}/_{T}T^{G}/_{T}^{G}/_{A}CA^{G}/_{A}CA$) (SEQ ID No, 4) were derived from amino-terminal protein sequence corresponding to residues 3-8 (CYNCIN) of pig CD59 and a region of high inter-species homology of all known CD59 sequences close to the C-terminus corresponding to residues 63-68 (SEQ ID NO: 23) (CCKKDL) in human CD59. The approximate positions of these primers are shown in the schematic diagram of the pig CD59 cDNA (Figure 1). A variation on the touchdown procedure of Don *et al* Nucleic Acids Res. 19:4008 was performed, with 500ng of each primer used in the amplification. A denaturation at 95°C for 4 minutes was followed by initial cycling parameters of 94°C for 30s, 54° for 40s and 72°C for 45s. Thereafter the annealing temperature of the reaction was decreased 2°C every second cycle from 54°C to a touchdown of 40°C at which temperature 25 cycles were carried out.—-

Replace the paragraph beginning at page 42, line 26, with the following rewritten paragraph:

--Amino-terminal sequencing was obtained through the

first 14 residues, 12 of which were identified with confidence. The sequence (SEQ ID NO: 24) (DCGLPPxVPxAQPA) was highly homologous with the amino terminal sequence of human DAF. Partial cDNA sequence has been obtained using a PCR-based approach with a primer designed from the above sequence and from internal protein sequences predicted from comparisons of DAF sequences in human, mouse, rat (our original data) and guinea pig to be highly conserved. The cDNAs so obtained have been labelled and used as probes to isolate full-length pig DAF cDNA clones from a pig testis cDNA library.--